

What is claimed is:

1. A method for determining a sequence boundary, comprising:

- 5 (a) contacting a population of addressed fragments of eukaryotic genomic DNA with a target polynucleotide, said target polynucleotide binding a terminal sequence of a DNA region, said addressed fragments of eukaryotic genomic DNA being at least 100  
10 nucleotides in length;
- (b) determining a relative order for 2 or more of said addressed fragments compared to a sequence of said genomic DNA;
- (c) identifying a pair of fragments among said  
15 2 or more addressed fragments that alternatively bind said terminal sequence of a region; and
- (d) determining for said sequence of said genomic DNA a relative location of a boundary of said region compared to a location of at least one genomic DNA  
20 fragment in said pair.

2. The method of claim 1, wherein said boundary separates an exon from an intron.

3. The method of claim 1, wherein said target polynucleotide comprises cDNA.

25 4. The method of claim 1, wherein said target polynucleotide comprises RNA.

5. The method of claim 1, wherein said addressed fragments of eukaryotic genomic DNA are surface bound.

6. The method of claim 5, wherein said surface is a particle.

7. The method of claim 5, wherein said surface is a location on an array.

5 8. The method of claim 1, wherein said pair of fragments have a portion of overlapping sequence.

9. The method of claim 1, wherein said pair of fragments have a portion of adjacent sequence compared to said sequence of said genomic DNA.

10 10. The method of claim 1, wherein said addressed fragments of eukaryotic genomic DNA are at least 200 nucleotides in length.

11 11. The method of claim 1, wherein said addressed fragments of eukaryotic genomic DNA are at  
15 least 500 nucleotides in length.

12. The method of claim 1, wherein said addressed fragments of eukaryotic genomic DNA are at least 1000 nucleotides in length.

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13. A method for determining a sequence boundary, comprising:

- (a) contacting a population of surface-bound fragments of eukaryotic genomic DNA with a target polynucleotide, said target polynucleotide binding a terminal sequence of a DNA region, said addressed fragments of eukaryotic genomic DNA being at least 100 nucleotides in length;
- (b) determining a relative order for 2 or more of said surface-bound fragments compared to a sequence of said genomic DNA;
- (c) identifying a pair of fragments among said 2 or more surface-bound fragments that alternatively bind said terminal sequence of a region; and
- (d) determining for said sequence of said genomic DNA a relative location of a boundary of said region compared to a location of at least one genomic DNA fragment in said pair.

14. The method of claim 13, wherein said boundary separates an exon from an intron.

15. The method of claim 13, wherein said target polynucleotide comprises cDNA.

16. The method of claim 13, wherein said target polynucleotide comprises RNA.

17. The method of claim 13, wherein said addressed fragments of eukaryotic genomic DNA are surface bound.

18. The method of claim 17, wherein said surface is a particle.

19. The method of claim 17, wherein said surface is a location on an array.

5 20. The method of claim 13, wherein said pair of fragments have a portion of overlapping sequence.

21. The method of claim 13, wherein said pair of fragments have a portion of adjacent sequence compared to said sequence of said genomic DNA.

10 22. The method of claim 13, wherein said addressed fragments of eukaryotic genomic DNA are at least 200 nucleotides in length.

23. The method of claim 13, wherein said addressed fragments of eukaryotic genomic DNA are at  
15 least 500 nucleotides in length.

24. The method of claim 13, wherein said addressed fragments of eukaryotic genomic DNA are at least 1000 nucleotides in length.

25. A method for determining a plurality of sequence boundaries, comprising:

- (a) contacting a population of addressed fragments of eukaryotic genomic DNA with a target polynucleotide, said target polynucleotide binding a plurality of terminal sequences of DNA regions, said addressed fragments of eukaryotic genomic DNA being at least 100 nucleotides in length;
- (b) determining a relative order for 2 or more of said addressed fragments compared to a sequence of said genomic DNA for a plurality of sets of 2 or more genomic DNA fragments;
- (c) identifying a plurality of pairs of fragments among said plurality of sets of 2 or more addressed fragments, said pairs comprising fragments that alternatively bind said terminal sequences of regions; and
- (d) determining for said sequence of said genomic DNA relative locations of boundaries for a plurality of said regions compared to locations of at least one genomic DNA fragment in each of said pairs.

26. The method of claim 25, wherein said boundaries separate exons from intron.

27. The method of claim 25, wherein said target polynucleotide comprises cDNA.

28. The method of claim 25, wherein said target polynucleotide comprises RNA.

29. The method of claim 25, wherein said addressed fragments of eukaryotic genomic DNA are surface bound.

30. The method of claim 29, wherein said  
5 surface is a particle.

31. The method of claim 29, wherein said surface is a location on an array.

32. The method of claim 25, wherein said pairs of fragments have portions of overlapping sequence.

10 33. The method of claim 25, wherein said pairs of fragments have portions of adjacent sequence compared to said sequence of said genomic DNA.

34. The method of claim 25, wherein said addressed fragments of eukaryotic genomic DNA are at  
15 least 200 nucleotides in length.

35. The method of claim 25, wherein said addressed fragments of eukaryotic genomic DNA are at least 500 nucleotides in length.

36. The method of claim 25, wherein said  
20 addressed fragments of eukaryotic genomic DNA are at least 1000 nucleotides in length.